

X380 #1
SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: WALLACH, DAVID
NOPHAR, YARON
KEMPER, OLIVER
ENGELMANN, HARTMUT
BRAKEBUSCH, CORD
ADERKA, DAN

(ii) TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
NECROSIS FACTOR BINDING PROTEIN I (TBP-I)

(iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/625668
(B) FILING DATE: 13-DEC-1990
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 256..1620

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 319..1620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGCCAGTG ATCTTGAACC CCAAAGGCCA GAACTGGAGC CTCAGTCCAG AGAATTCTGA	60
GAAAATTAAA GCAGAGAGGA GGGGAGAGAT CACTGGGACC AGGCCGTGAT CTCTATGCC	120
GAGTCTCAAC CCTCAACTGT CACCCCAAGG CACTTGGGAC GTCCTGGACA GACCGAGTCC	180
CGGGAAGCCC CAGCACTGCC GCTGCCACAC TGCCCTGAGC CCAAATGGGG GAGTGAGAGG	240
CCATAGCTGT CTGGC ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCG	291
Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro	
-21 -20 -15 -10	
CTG GTG CTC CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT	339
Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile	
-5 1 5	
GGA CTG GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT	387
Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys	
10 15 20	
CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC	435
Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr	
25 30 35	
AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG GGG	483
Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly	
40 45 50 55	

CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC GCT TCA Gln Asp Thr Asp Cys Arg Glu Cys Ser Gly Ser Phe Thr Ala Ser	531
60 65 70	
GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA TGC CGA AAG GAA Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu	579
75 80 85	
ATG GGT CAG GTG GAG ATC TCT TGC ACA GTG GAC CGG GAC ACC GTG Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val	627
90 95 100	
TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT TGG AGT GAA AAC CTT Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu	675
105 110 115	
TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT GGG ACC GTG CAC CTC Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu	723
120 125 130 135	
TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC ACC TGC CAT GCA GGT TTC Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe	771
140 145 150	
TTT CTA AGA GAA AAC GAG TGT GTC TCC TGT AGT AAC TGT AAG AAA AGC Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser	819
155 160 165	
CTG GAG TGC ACG AAG TTG TGC CTA CCC CAG ATT GAG AAT GTT AAG GGC Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly	867
170 175 180	
ACT GAG GAC TCA GGC ACC ACA GTG CTG TTG CCC CTG GTC ATT TTC TTT Thr Glu Asp Ser Gly Thr Val Leu Leu Pro Leu Val Ile Phe Phe	915
185 190 195	
GGT CTT TGC CTT TTA TCC CTC ATT GGT TTA ATG TAT CGC TAC Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr	963
200 205 210 215	
CAA CGG TGG AAG TCC AAG CTC TAC TCC ATT GTT TGT GGG AAA TCG ACA Gln Arg Trp Lys Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr	1011
220 225 230	
CCT GAA AAA GAG GGG GAG CTT GAA GGA ACT ACT ACT AAG CCC CTG GCC Pro Glu Lys Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala	1059
235 240 245	
CCA AAC CCA AGC TTC AGT CCC ACT CCA GGC TTC ACC CCC ACC CTG GGC Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly	1107
250 255 260	

TTC	AGT	CCC	GTG	CCC	AGT	TCC	ACC	TTC	ACC	TCC	AGC	TCC	ACC	TAT	ACC	1155
Phe	Ser	Pro	Val	Pro	Ser	Ser	Thr	Phe	Thr	Ser	Ser	Ser	Thr	Tyr	Thr	
265				270						275						
CCC	GGT	GAC	TGT	CCC	AAC	TTT	GCG	GCT	CCC	CGC	AGA	GAG	GTG	GCA	CCA	1203
Pro	Gly	Asp	Cys	Pro	Asn	Phe	Ala	Ala	Pro	Arg	Arg	Glu	Val	Ala	Pro	
280				285					290					295		
CCC	TAT	CAG	GGG	GCT	GAC	CCC	ATC	CTT	GCG	ACA	GCC	CTC	GCC	TCC	GAC	1251
Pro	Tyr	Gln	Gly	Ala	Asp	Pro	Ile	Leu	Ala	Thr	Ala	Leu	Ala	Ser	Asp	
				300				305					310			
CCC	ATC	CCC	AAC	CCC	CTT	CAG	AAG	TGG	GAG	GAC	AGC	GCC	CAC	AAG	CCA	1299
Pro	Ile	Pro	Asn	Pro	Leu	Gln	Lys	Trp	Glu	Asp	Ser	Ala	His	Lys	Pro	
				315				320					325			
CAG	AGC	CTA	GAC	ACT	GAT	GAC	CCC	GCG	ACG	CTG	TAC	GCC	GTG	GTG	GAG	1347
Gln	Ser	Leu	Asp	Thr	Asp	Asp	Pro	Ala	Thr	Leu	Tyr	Ala	Val	Val	Glut	
		330				335					340					
AAC	GTG	CCC	CCG	TTG	CGC	TGG	AAG	GAA	TTC	GTG	CGG	CGC	CTA	GGG	CTG	1395
Asn	Val	Pro	Pro	Leu	Arg	Trp	Lys	Glu	Phe	Val	Arg	Arg	Leu	Gly	Leu	
		345				350					355					
AGC	GAC	CAC	GAG	ATC	GAT	CGG	CTG	GAG	CTG	CAG	AAC	GGG	CGC	TGC	CTG	1443
Ser	Asp	His	Glu	Ile	Asp	Arg	Leu	Glu	Leu	Gln	Asn	Gly	Arg	Cys	Leu	
		360				365				370			375			
CGC	GAG	GCG	CAA	TAC	AGC	ATG	CTG	GCG	ACC	TGG	AGG	CGG	CGC	ACG	CCG	1491
Arg	Glu	Ala	Gln	Tyr	Ser	Met	Leu	Ala	Thr	Trp	Arg	Arg	Arg	Thr	Pro	
				380				385					390			
CGG	CGC	GAG	GCC	ACG	CTG	GAG	CTG	CTG	GGA	CGC	GTG	CTC	CGC	GAC	ATG	1539
Arg	Arg	Glu	Ala	Thr	Leu	Glu	Leu	Leu	Gly	Arg	Val	Leu	Arg	Asp	Met	
				395				400					405			
GAC	CTG	CTG	GGC	TGC	CTG	GAG	GAC	ATC	GAG	GAG	GCG	CTT	TGC	GGC	CCC	1587
Asp	Leu	Leu	Gly	Cys	Leu	Glu	Asp	Ile	Glu	Glu	Ala	Leu	Cys	Gly	Pro	
		410				415					420					
GCC	GCC	CTC	CCG	CCC	GCG	CCC	AGT	CTT	CTC	AGA	TGAGGCTGCG	CCCTGCGGGC				1640
Ala	Ala	Leu	Pro	Pro	Ala	Pro	Ser	Leu	Leu	Arg						
		425				430										
AGCTCTAAGG	ACCGTCCTGC	GAGATCGCCT	TCCAACCCA	CTTTTTCTG	GAAAGGAGGG											1700
GTCCTGCAGG	GGCAAGCAGG	AGCTAGCAGC	CGCCTACTTG	GTGCTAACCC	CTCGATGTAC											1760
ATAGCTTTTC	TCAGCTGCCT	GCGCGCCGCC	GACAGTCAGC	GCTGTGCGCG	CGGAGAGAGG											1820

TGCGCCGTGG GCTCAAGAGC CTGAGTGGGT GGTTTGCAG GATGAGGGAC GCTATGCC	TC	1880
ATGCCCGTT TGGGTGTCCT CACCAGCAAG GCTGCTCGGG GGCCCCTGGT TCGTCCCTGA		1940
GCCTTTTCA CAGTGCATAA GCAGTTTTT TTGTTTTGT TTTGTTTTGT TTTGTTTTA		2000
AATCAATCAT GTTACACTAA TAGAAACTTG GCACTCCTGT GCCCTCTGCC TGGACAAGCA		2060
CATAGCAAGC TGAACGTGCC TAAGGCAGGG GCGAGCACGG AACAAATGGGG CCTTCAGCTG		2120
GAGCTGTGGA CTTTGTACA TACACTAAAA TTCTGAAGTT AAAAAAAA AAAAA		2175

(2) INFORMATION FOR SEQ ID NO:2:

- O*
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 455 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu							
-21 -20							-10
Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro							
-5							10
His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys							
15							25
Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys							
30							40
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp							
45							55
Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu							
60							75
Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val							
80							90
Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg							
95							105
Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe							
110							120

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
125 130 135

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
140 145 150 155

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
160 165 170

Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
175 180 185

Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
190 195 200

Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
205 210 215

Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
220 225 230 235

Gly Glu Leu Glu Gly Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
240 245 250

Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
255 260 265

Pro Ser Ser Thr Phe Thr Ser Ser Thr Tyr Thr Pro Gly Asp Cys
270 275 280

Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
285 290 295

Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
300 305 310 315

Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
320 325 330

Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
335 340 345

Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
350 355 360

Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
365 370 375

Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
380 385 390 395

Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
400 405 410

Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
415 420 425

Pro Ala Pro Ser Leu Leu Arg
430

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGNGTYCCNT TYATRTARGT DGGNGT

26

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGNGTYCCNT TYATRTA

17

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTYATRTARG TDGGNGT

17

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGGCCGATGG GCCTCTCCAC CGTGCCT

27

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATAGTATTCTAACATCTGGGTAGGCA

27

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asp Ser Val Cys Pro
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AATTCAATGGA TAGTGTGTGT CCC

23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTACCTATCA CACACAGGGG TTC

23

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys
1 5 10 15

Arg Leu Arg Glu Tyr Tyr
20

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Leu Cys Ala Pro Leu Arg Lys
1 5

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Cys Arg Pro Gly Phe Gly Val Ala Arg
1 5

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Cys Gly Pro Ser Tyr Pro Asp
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Pro Gly Trp Tyr Cys Ala Leu Ser Lys
1 5

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys
1 5 10 15

Arg

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Cys Arg Pro Gly Phe Gly Val Ala Arg
1 5

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly
1 5 10 15

Thr Phe Ser Lys
20

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Cys Arg Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp
1 5 10 15

Val Val Cys Lys
20

(2) INFORMATION FOR SEQ ID NO:26:

- (1)* SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln
1 5 10 15

Leu Trp

TABLE 1: Amino Acid Sequences of TBP I and TBP II

TBP I: CNBr-1 (=N-terminus)	NH ₂	Asp	Ser	Val	Cys	Pro	Gln	Gly	Lys	Tyr	Ile	His	Pro	Gln	-		
(Seq. ID No.: 2, amino acids 41-53)																	
CNBr-2	NH ₂	Gly	Gln	Val	Glu	Ile	Ser	Ser	Cys	Thr	Val	Asp	Arg	Asp	Thr	Val	
	(Seq. ID No.: 2, amino acids 110-124)																
C-terminus	-	Ile	Glu	Asn	COOH												
TBP III: N-terminus	(Seq. ID. No. 11)	NH ₂	Ala	Gln	Val	Ala	Phe	Thr	Pro	Tyr	Ala	Pro	Glu	Pro	Gly	Ser	Thr
TRP 35	(Seq. ID. No. 12)	NH ₂	Leu	Cys	Arg	Leu	Arg	Glu	Tyr	Tyr	-						
TRP 39/1	(Seq. ID. No. 13)	NH ₂	Cys	Arg	Pro	Ala	Pro	Leu	Arg	Lys							
TRP 39/2	(Seq. ID. No. 14)	NH ₂	Glu	Tyr	Tyr	Asp	Gln	Thr	Ala	Gln	Met	Cys	Cys	-			
TRP 44/1	(Seq. ID. No. 15)	NH ₂	Glu	Tyr	Tyr	Asp	Gln	Thr	Ala	Gln	Met	Cys	Cys	Ser	-		
TRP 44/2	(Seq. ID. No. 16)	NH ₂	Ser	Cys	Gly	Pro	Ser	Tyr	Pro	Asp	-						
TRP 46/1	(Seq. ID. No. 17)	NH ₂	Phe	Thr	Pro	Tyr	Ala	Pro	Glu	Pro	Gly	Ser	Thr	Cys	Arg	-	
TRP 46/2	(Seq. ID. No. 18)	NH ₂	Leu	Arg	Glu	Tyr	Tyr	Asp	Gln	Thr	Ala	Gln	Met	Cys	Cys	-	
TRP 50	(Seq. ID. No. 18)	NH ₂	Leu	Arg	Glu	Tyr	Tyr	Asp	Gln	Thr	Ala	Gln	Met	Cys	Cys	-	
TRP 54/1	(Seq. ID. No. 19)	NH ₂	Pro	Gly	Trp	Tyr	Cys	Ala	Leu	Ser	Lys						
TRP 54/2	(Seq. ID. No. 20)	NH ₂	Ala	Gln	Val	Ala	Phe	Thr	Pro	Tyr	Ala	Pro	Glu	Pro	Gly	Ser	Thr
TRP 53/1	(Seq. ID. No. 21)	NH ₂	Val	Ala	Phe	Thr	Pro	Tyr	Ala	Pro	Glu	Pro	Gly	Ser	Thr	Cys	Arg
TRP 53/2	(Seq. ID. No. 22)	NH ₂	Cys	Arg	Pro	Gly	Phe	Gly	Val	Ala	Arg						
TRP 60	(Seq. ID. No. 23)	NH ₂	Ile	Cys	Thr	Cys	Arg	Pro	Gly	Trp	Tyr	Cys	Ala	Ile	Ser	-	
TRP 62	(Seq. ID. No. 24)	NH ₂	Pro	Gly	Thr	Glu	Thr	Ser	Asp	Val	Val	Cys	Lys	Pro	Cys	Ala	Pro
TRP 65	(Seq. ID. No. 24)	NH ₂	Gly	Thr	Phe	Ser	Lys										
TRP 67	(Seq. ID. No. 25)	NH ₂	Gly	Thr	Phe	Ser	Lys										
TRP 84	(Seq. ID. No. 26)	NH ₂	Cys	Arg	Pro	Gly	Phe	Gly	Val	Ala	Arg	Pro	Gly	Thr	Glu	Thr	Ser
			Asp	Val	Cys	Lys											

Gln Leu Trp -